

APR 24 1998

PATENT

ATTORNEY DOCKET NO. A21-535.1007  
07148/032001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Lorin R. DeBonte et al.  
Serial No.: 08/572,027  
Filed : December, 14, 1995  
Title : PLANTS HAVING MUTANT SEQUENCES THAT CONFER ALTERED  
FATTY ACID PROFILES

Art Unit: 1649  
Examiner: G. Benzion

Assistant Commissioner for Patents  
Washington, DC 20231

DECLARATION UNDER 37 CFR §1.132 OF GUO-HUA MIAO

I, Guo-Hua Miao, declare as follows:

1. That I am a citizen of the People's Republic of China and presently live at 202 Cherry Blossom Place, Hockessin, Delaware.

2. That I received a Bachelor of Science degree in Biology from Shanghai Normal University, Shanghai, China in 1982, a Master of Science degree in Plant Physiology from Shanghai Institute of Plant Physiology, Chinese Academy of Science, Shanghai, China in 1984 and a Doctor of Philosophy degree in Molecular, Cellular and Developmental Biology from Ohio State University, Columbus, Ohio in 1991.

3. That I was employed as a research associate at the Biotechnology Center, Ohio State University, Columbus, Ohio from 1991 to 1993.

4. That I am presently employed as a Senior Research Molecular Biologist by DuPont Agricultural Products, a division of E. I. Dupont de Nemours, Inc. and have been so employed since 1993.

5. That, as an employee of DuPont, I determined Fad2 desaturase coding sequences obtained from canola lines Westar and Q508. Westar is a canola variety having no known mutations in

Declaration of Guo-Hau Miao  
Serial No. 08/572,027

Fad2 desaturase genes. Q508 is a line derived from Westar by mutagenesis. A copy of four microfilmed pages from my laboratory notebook is attached as Exhibit A (Notebook F79066, pages 140-143). These notebook pages show the DNA sequences and deduced amino acid sequences that were obtained by me or under my supervision. The dates on these four pages, all of which are prior to December 14, 1995, have been blocked out.

The DNA and deduced amino acid sequence of Fad2-F from line Q508 is shown at pages 140-141. The Q508 Fad2-F sequence contains a mutation at nucleotide 515 compared to the wild-type Westar sequence, as indicated at page 140 of the notebook. The wild-type nucleotide at this position is T, and the mutant nucleotide is A. Based on the information at pages 140-141, the mutant Q508 Fad2-F and wild-type Fad2-F sequences contain a G at position 316.

The DNA and deduced amino acid sequences of Fad2-D from the Westar variety is shown at pages 142-143. The wild-type Fad2-D sequence contains a G at nucleotide 316, whereas the IMC 129 mutant Fad2-D sequence contains an A, as indicated at page 142 of the notebook. Based on the information at pages 142-143, the wild-type Fad2-D and mutant IMC 129 Fad2-D sequences contain a T at position 515.

6. After these sequences were determined, the mutant Fad2-D sequence and the mutant Fad2-F sequence were mailed to Ronald Lundquist. A copy of the sequences that were mailed, as well as the cover letter, are attached hereto as Exhibit B. The dates on these pages, all of which are prior to December 14, 1995, have been blocked out. A comparison of the nucleotide sequences in my laboratory notebook to those enclosed with the letter to Ronald Lundquist indicates that the sequences enclosed in the letter were incorrectly labeled. The sequence labeled as "f-gene, 508" corresponds to the wild-type Fad2-D sequence of my

Declaration of Guo-Hau Miao  
Serial No. 08/572,027

notebook, with the Q508 mutation inserted at position 515. The sequence labeled as "d-gene, 129" corresponds to the wild-type Fad2-F sequence of my notebook, with the IMC 129 mutation inserted at position 316. It appears that the sequence labels were inadvertently switched and the D and F mutations added to the sequence prior to mailing the information to Mr. Lundquist.

7. I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the instant patent application or any patent issuing thereon.

Dated: 10/1/98

  
Guo-Hua Miao, Ph.D.

14066.M11

# E. I. DUPONT DE NEMOURS AND COMPANY

140

Page No.      TITLE

Conf'd from Page 1

**DATE**

5 79066

Book No.      PURPOSE

Book No. PURPOSE Cont'd from page 153

5 10 15 20 25 30 35 40 45  
 ATG GGT GCA GTT GCA AGA ATG CAA GTG TCT CCT CCC TCC AAC AAC AAC TCT  
 TAG CCA CGT CCA CCT TCT TAC GTT CAC AGA GGA GGG AGG TTC TTC ACA  
 M G A G G R M Q V S P P S K X S >  
 50 55 60 65 70 75 80 85 90 95  
 GAA ACC GAC ACC ATC AAG CGC CTA CCC TCC GAG ACA CCG CCC TTC ACT  
 CCT TGG CTC TGG TAG TTC GGC CAT GGG AGC CTC TGT GGC GGG AAC TCA  
 E T D T I X R V P C E T P F P F D  
 100 105 110 115 120 125 130 135 140  
 GTC GCA GAA CTC AAC AAA GCA ATC CCA CGG CAC TGT TTC AAA CGC TCG  
 CGC CCT CCT GAG TGG TTT CCT TGG GGT GGC GTG ACA AAC TTT GCG AGC  
 V G E L K K A I P P H C F K R S >  
 145 150 155 160 165 170 175 180 185 190  
 ATC CCT CGC TCT TIC TCC TAC CTC ATC TGG GAC ATC ATC ATA GGC TCC  
 TAG GGA CGC AGA AAG AGG ATG GAG TAG AAC CTG TAG TAG TAT CGG AGG  
 I P R S F S Y L I W D I I I I A >  
 195 200 205 210 215 220 225 230 235 240  
 TGC TTC TAC TAC NTC GGC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT  
 AGC AAG ATG ATG NAG CGG TGG TGA ATG AAG GGA GAG GAG GCA GTG GGA  
 C F Y Y X A T I Y F P L L B H P >  
 245 250 255 260 265 270 275 280 285  
 CTC TCC TAC TTC GGC TGG CCT CTC TAC TGG GGC TGC CAA CGG TGC GTC  
 GAG AGG ATG AAG CGG ACC GGA GAG ATG ACC CGG AGC GTT CCC AGC CAG  
 L S Y F A W P L Y N A C [REDACTED]  
 290 295 300 305 310 315 320 325 330 335  
 CTA ACC CGC GTC TGG GTC ATA GCC CAC GAG TGC GGC GAC CAC GGC TIC  
 CAT TGG CGG CAG ACC CAG TAT CGG GTG CTC ACG CGG GTG GTG CGG AAC  
 [REDACTED] T G Y V A [REDACTED]  
 340 345 350 355 360 365 370 375 380  
 ACC GAC TAC CGG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC  
 TGG CTG ATG GTC ACC GAA CTG CTG TGG CAG CCA GAG TAG AAG GTG AGC  
 I S D Y Q W L D D T V G L ! F H S >  
 385 390 395 400 405 410 415 420 425 430  
 TTC CTC CTC GTC CCT TAC TTC TCC TGG AGG TAC ATG CAT CGC AGC CAC  
 AAG GAG CGG CGG GGA ATG AAG AGC ACC TTC ATG TCA GIA GCG TCC GTG  
 F L L V P Y F S W K Y S H R S H >  
 435 440 445 450 455 460 465 470 475 480  
 CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAC  
 GTC AGG TGG TGA CCG AGG GAG CTC TCT CTC GTT CAT AAC AAA CAG GGG TIC  
 H S V I G S L E R D E V F V P K >  
 485 490 495 500 505 510 (L) - 520 525 529  
 AAG AAC TCA GAC ATC AAG TGG TAC GGC AAC AGG TAG AAC CAC AAC AAC CCT TIG  
 TIC TTC AGT CTG TAG TTC ACC ATG CCG TTC ATG GTG TIG TIG GGA AAC  
 K K S D I K W Y C K Y H N N P L >  
 530 535 540 545 550 555 560 565 570 575  
 GGA CGC ACC GTG ATG TTA AGC GTT CAG TTC ACT CTC GGC TGG CGG TIG  
 CCT GCG TGG CAC TAC AAC TGC CAA GTC AAC TCA CAC CGG AGC GGC AAC  
 G R T V M L T V Q F T L G W P L >  
 580 585 590 595 600 605 610 615 620  
 TAC TTA GGC TTC AAC GTC TCG GCA AGA CCT TAC GAC CGC GGC TTC CCT  
 ATG ATC CGG AGG TGG CAG AGC CCT TCT GGA ATG CTC CGG CCT AAC GCA  
 I L A E V D G P F T D G F E R >

## DNA and Lederer

~~protozoa~~ *spores*

of Santa Fe

(P) from Q5t.

~~It was found~~

~~in water and~~

129 changes.

~~Class is 4508~~

## ~~a history~~

replaces locline  
position 514-516 bp

This mutation

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~~is speaking~~

Chancery

42508

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Region w<sub>4</sub> 3

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Page No.

141

PURPOSE

*cont'd*

Book No.

F 79066

625 630 635 640 645 650 655 660 665 670  
 TCC CAT TTC CAC CGC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC  
 ACG GTA AAG GTG GGG TTG CGA CGG TAG ATG TTG CTG CGG CTC GCA GAG  
 C H F K P N A P I Y N D R E R L  
 675 680 685 690 695 700 705 710 715 720  
 CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC CGC GTC TAC GCT CTC  
 GTC TAT ATG TAG AGG CTG CGA CGG TAG GAG CGG CAG ACG ATG CCA GAG  
 Q I Y Z S D A G I L A V C Y G L  
 725 730 735 740 745 750 755 760 765  
 TTC CGT TAC CGC CGG CGG CGA GTG GGC TCC ATG GTC TCC TAC  
 AAG CGA ATG CGG CGG CGG CCT CCT CGC CGG AGC TAC CAC AGG AAG ATG  
 P R Y A A G Q G V A S M V C F Y  
 770 775 780 785 790 795 800 805 810 815  
 GGA GTC CGG CCT CTG ATT GTC ATT GGT TTC CTC GTG TAC ACT TAC  
 CCT CGG CGG GAA GAC TAA CGG TTA CGA AAG GAG CAC AGC TAG TGA ATG  
 G V P L L I V N G F L V L I T Y  
 820 825 830 835 840 845 850 855 860  
 TTG CAG CAC ACC GAT CCT TCC CTG CCT CAC TAG GAT TCG TCC GAG TGG  
 AAC GTC GTG TGC GAA AGG GAC CGA GTG ATG CTA AGC AGG CCT ACC  
 L Q H T H P S L P H Y D S S E W  
 865 870 875 880 885 890 895 900 905 910  
 GAT TGG TTC AGG GGA GCT TTG GCT ACC CCT GAC AGA GAC TAC GGA ATC  
 CTA ACC AAG TCC CCT CGA AAC CGA TGG CGA CCT TCT GTG ATG CCT TAG  
 D W F R G A L A T V D R D Y G Y  
 915 920 925 930 935 940 945 950 955 960  
 TTG AAC AAG GTC TTC CAC ATT ATT ACC GAC AAG GAC GTG GCC CAT CAT  
 AAC TTG TTC CAG AAC GTG TTA TAA TGG CGC TGC GTG GAC CGG GTA GTC  
 L N K V F H N I T D T H V A H H  
 965 970 975 980 985 990 995 1000 1005  
 CCG TTC TCC ACG ATG CGG CAT TAT CAC CGU ATG GAA GCT ACC AAG GCG  
 GGC AAC AGG TGC TAC CGC GTA ATA GTG CGG TAC CCT CGA TGG TTC CGC  
 P F S T M P H Y H A M E A T R A  
 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055  
 ATA AAG CGG ATA CTG GGA CAC TAT TAT CAC TTC GAT GGG AGG CGG GTG  
 ATT TTC GGC TAT GAC CCT CCT ATA ATA GTG AAG CTA CCC TGC GGC CAC  
 I K P I L G E Y Y Q F D G T P V  
 1060 1065 1070 1075 1080 1085 1090 1095 1100  
 GTT AAG CGG ATG TGG AGG GAG CGG AAG GAG TGT ATC DAT GTG GAA CGG  
 CAA CGT CGC TAC CGC TCC CCT CGG TTC CTC ACA TAG ATA CGC CCT CGC  
 V K A M W R E A K E C I Y V E P  
 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150  
 GAC AGG CGA GGT GAG AAC AAA GGT GTG TTC TGG TAC AAC ATT AAC TTA  
 CGT TCC GTT CGA CCT CTC TTC CCT CGC AAC AAC AGC ATG TGC TTA TCC ATT  
 D R Q G E K K G V F W Y N N K L  
 1155 1160 1165 1170 1175 1180 1185  
 TGA GCA ATT GAT GAT GGT GAA AGA ATT CAC TAG  
 ACT CCT ATA CTA CTA CCT CCT TTA GTG ATC  
 \* G Y D D G E R N H \*

*See prime location**on page 134**In Q508**a Mai S.L.**was last seen**on the sequence**analysis.**CCTC (cont'd)**(CAC 605-E)**Mai + T (CCTC)**Therefore, Mai**will provide a**simple way to**distinguish Q508**and AT + TG.*

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*Smith Jr.*

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E. I. DUPONT DE NEMOURS AND COMPANY

142

Page No. 三

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E 79066

**Book No.      PURPOSE**

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DNA and deduced  
protein sequences  
from vector FAD2

• 60

In 129 and

Q 506 class

$\leftarrow$  was converted  
to  $MR\leftarrow(k)$

~~This note~~

Digitized by srujanika@gmail.com

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to bat occur

in both 129 and

~~Q508 mutant~~

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~~Agave~~ - ~~ily~~

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## E. I. DUPONT DE NEMOURS AND COMPANY

TITLE conf'd DATE \_\_\_\_\_ Page No. 143  
 PURPOSE conf'd Book No. E 79066

625	630	635	640	645	650	655	660	665	670
TGC CAT TTC CGC CCC AAC GCT CCC ATG TAG AAC GAC GCG GAG CGT CTC									
ACG GTA AAG GTG CGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG									
C H E H P N A P I Y N D R E R L>									
675	680	685	690	695	700	705	710	715	720
CGG ATA TAC ATC TCC GAC GCT GGC ATC CTC GGC GTC TAC TAC GCT CTC									
GTC TAT ATG TAG AGG CTG CGA CGG TAG CGC CGG CGG ACC ATG CCA CAG									
Q I Y I S D A C I L A V C T G L>									
725	730	735	740	745	750	755	760	765	
TAC CGG TAC GCT GGT GTC CAA CGA GGA GTT GCG TCC ATG GTC TGC TTC TAC									
ATG GGG ATG CGA CGA CAG GTT CCT CAA CGC ACC TAC CAG ACC AAG ATG									
Y R T A A V Q G V A S M V C F Y>									
770	775	780	785	790	795	800	805	810	815
GGA GTT CGG CCT CTG ATT GTC AAT GGG TTG TTA GTT TTG ATG ACT TAC									
CCT CAA CGC GAA GAC TAA CGG TTA CGG AAG AAT CAA AAC TAG TGA ATG									
G U P L L I V N G F L V L I T Y>									
820	825	830	835	840	845	850	855	860	
TTC CAQ CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCC TCT GAG TGG									
AAC GTC GTG TGC GTA CGA AGG GAC CGA GTG ATA CTG ACC AGA CTC ACC									
L Q H T H P S L P H Y D S S E W>									
865	870	875	880	885	890	895	900	905	910
GAT TGG TTG AGG CGG GCA GCT TTG CGC ACC GTT GAC AGA GAC TAC CGA ATC									
CTA ACC AAC TCC CCT CGA AAC CGG TGC CGA CTG CCT ATG CCT TAC TAC									
D W L R G A L A T V D R D Y G L>									
915	920	925	930	935	940	945	950	955	960
TTG AAC AAG GTC TTC CAC AAT ATC ACC GAC AGC CAC GTC CGG CAT CAC									
AAC TTG TTC CAG AAG GTG TTA TAG TGC CTG TCC GTG CAC CGC GTC GTG									
L N K V F H N I T D T H V A H H>									
965	970	975	980	985	990	995	1000	1005	
CTG TTC TCG ACC ATG CGG CAT TAT CAT CGG ATG GAA GCT ACC AAG CGG									
GAC AAG AGC TGG TAC CGC GTC ATA GTC CGC TAC CCT CGA TCC TTC CGG									
L F S T M P H Y H A M K A T K A>									
1010	1015	1020	1025	1030	1035	1040	1045	1050	1055
ATA AAG CGG ATA CTG CGA GAG TAT TAT CAC TTG CAT CGG AGC CGG STG									
TAT TTG CGC TAT GAC CCT CTC ATA ATA GTC AAC GTC CCC TCC CGC CAC									
I K P I L G E Y Y Q L H G T P V>									
1060	1065	1070	1075	1080	1085	1090	1095	1100	
GTT AAC CGG ATG TGC ACC AGG GAG CGG AAC GAG TGT ATC TAT GTG GAA CGG									
CAA TAC CGG TAT ACC TCC CCT CGC TTC ACA TAC ATA CGC CCT CGC									
V K A M W R E A K E C I Y V E P>									
1105	1110	1115	1120	1125	1130	1135	1140	1145	1150
CAC AGG CGA GGT GAG AAC AAA GGT CGC TTG TGG TAC AAC AAT AAC TTA									
CTG TCC GTT CCA CGC TTC TTG CGA AAC AGC ATG TGG TTA TTC ATN									
D R Q G E K K G V F W Y N N X>									
1155	1160	1165	1170						
TCA AGC AAA GAA GAA ACA AT									
ACT TCC TTT CCT CCT TGT TA									
S K E E T Y>									

*weak streaky**(see page 134)**from prime location.**Total 5 segments**129 and 954**clones (each about**5m) were**sequenced by**prime DR**(see page 134)**and showed the*  
*same mutation.**Thus it appears**to be true**mutation.**This will be*  
*further confirmed*  
*by re RT-PCR*  
*and from 1st - 3rd*  
*and sequenced by*  
*DR primer*EXPERIMENTER George P. Jr.

DATE \_\_\_\_\_

WITNESSED BY C. Neppert

DATE \_\_\_\_\_



R E C I V E D

AGRICULTURAL PRODUCTS  
Experimental Station  
P.O. Box 80402  
Wilmington, Delaware 19880-0402

RONALD C. LUNDQUIST

Mr. Ronald Lundquist  
Fisher Richardson  
330 Dain Bosworth Tower  
60 S. 6th St.  
Minneapolis, Minnesota 55402

Dear Ron:

It was very nice speaking with you over the phone on Monday. I am sending you the information about the molecular analysis of IMC129 and IMCQ508 mutations, which you requested for IMC129 and IMCQ508 patent application. A disc containing the nucleotide sequences for both canola FAD2 genes (D and F) are also included.

As we discussed over the phone, IMCQ508 mutation was identified based on sequencing of cDNA clones isolated from IMCQ508 mutant, however, the mutation had not been confirmed as we did for IMC129 mutation. Therefore, we might need to further confirm the mutation, if we would like to include IMCQ508 in the patent application. Please feel free to contact me if I can provide you any additional information about the two mutants.

Sincerely,

Guo-Hua Miao, Ph.D.  
Research Molecular Biologist

CC: W. R. Majarian

Encl.

8:53 AM

5	10	15	20	*	25	30	*	35	40	*	45	50
*	*	*	*	*	*	*	*	*	*	*	*	*
ATGGGTGCAG GTGGAAGAAT GCAAGTGTCT CCTCCCTCCA AAAAGTCTGA												
TACCCACGTC CACCTTCITA CGTTCACAGA GGAGGGAGGT TTTTCAGACT												
55	60	65	70	*	75	80	*	85	90	*	95	100
*	*	*	*	*	*	*	*	*	*	*	*	*
AACCAGACAAC ATCAAGCGCG TACCCCTGCAG GACACCGCCC TTCACTGTGC												
TTGGCTGTTG TAGTTCGCGC ATGGGACGCT CTGTGGCGGG AAGTGACAGC												
105	110	115	120	*	125	130	*	135	140	*	145	150
*	*	*	*	*	*	*	*	*	*	*	*	*
GAGAACTCAA GAAAGCAATC CCACCCGCACT GTTTCAAACG CTCGATCCCT												
CTCTTGAGTT CTTTCGTTAG GGTGGCGTGA CAAAGTTGC GAGCTAGGGA												
155	160	165	170	*	175	180	*	185	190	*	195	200
*	*	*	*	*	*	*	*	*	*	*	*	*
CGCTCTTCT CCTACCTCAT CTGGGACATC ATCATAGCCT CCTGCTTCTA												
GCGAGAAAGA GGATGGAGTA GACCCTGTAG TAGTATCGGA GGACGAAGAT												
205	210	215	220	*	225	230	*	235	240	*	245	250
*	*	*	*	*	*	*	*	*	*	*	*	*
CTACGTCGCC ACCACTTACT TCCCTCTCCT CCCTCACCCCT CTCTCCTACT												
GATGCAGCGG TGGTGAATGA AGGGAGAGGA GGGAGTGGGA GAGAGGATGA												
255	260	265	270	*	275	280	*	285	290	*	295	300
*	*	*	*	*	*	*	*	*	*	*	*	*
TCGCCTGGCC TCTCTACTGG GCCTGCCAGG GCTGCGTCCT AACCGGCGTC												
AGCGGACCGG AGAGATGACC CGGACGGTCC CGACGCAGGA TTGGCCGCAG												
305	310	315	320	*	325	330	*	335	340	*	345	350
*	*	*	*	*	*	*	*	*	*	*	*	*
TGGGTCAAG CCCACAGTG CGGCCACAC GCCTTCAGCG ACTACCAGTG												
ACCCAGTATC GGGTGTCAC GCCGGTGGTG CGGAAGTCGC TGATGGTCAC												
355	360	365	370	*	375	380	*	385	390	*	395	400
*	*	*	*	*	*	*	*	*	*	*	*	*
GCTGGACGAC ACCGTCGGCC TCATCTTCCA CTCCCTCCTC CTCGTCCCTT												
CGACCTGCTG TGGCAGCCGG AGTAGAAGGT GAGGAAGGAG GAGCAGGGAA												
405	410	415	420	*	425	430	*	435	440	*	445	450
*	*	*	*	*	*	*	*	*	*	*	*	*
ACTTCTCCTG GAAGTACAGT CATCGACGCC ACCATTCAA CACTGGCTCC												
TGAAGAGGAC CTTCATGTCA GTAGCTGCGG TGGTAAGGTT GTGACCGAGG												
455	460	465	470	*	475	480	*	485	490	*	495	500
*	*	*	*	*	*	*	*	*	*	*	*	*
CTCGAGAGAG ACGAAGTGTG TGTCCCCAAG AAGAAGTCAG ACATCAAGTG												
GAGCTCTCTC TGCTTCACAA ACAGGGGTTT TTCTTCAGTC TGTAGTTCAC												
505	510	515	520	*	525	530	*	535	540	*	545	550
*	*	*	*	*	*	*	*	*	*	*	*	*
GTACGGCAAG TACCAACAA ACCCTTTGGG ACGCACCGTG ATGTTAACGG												
CATGCCGTTT ATGGAGTTGT TGGGAAACCC TGCGTGGCAC TACAATTGCC												
555	560	565	570	*	575	580	*	585	590	*	595	600
*	*	*	*	*	*	*	*	*	*	*	*	*
TTCAGTTCAC TCTCGGCTGG CCTTTGTACT TAGCCTTCATA CGTCTCGGGG												
AAGTCAAGTG AGAGCCGACC GGAAACATGA ATCGGAAGTT GCAGAGCCCC												
605	610	615	620	*	625	630	*	635	640	*	645	650
*	*	*	*	*	*	*	*	*	*	*	*	*
AGACCTTACG ACGGCGGCTT CGCTTGCCAT TTCCACCCCA ACGCTCCCCAT												

8:53 AM

TCTGGAATGC TGCCGCCGAA GCGAACGGTA AAGGTGGGGT TGCGAGGGTA

655	660	665	670	675	680	685	690	695	700
*	*	*	*	*	*	*	*	*	*
CTACAAACGAC	CGCGAGCGTC	TCCAGATATA	CATCTCCGAC	GCTGGCATCC					
GATGTTGCTG	GGCCTCGCAG	AGGTCTATAT	GTAGAGGCTG	CGACCGTAGG					
705	710	715	720	725	730	735	740	745	750
*	*	*	*	*	*	*	*	*	*
TCGCCGTCTG	CTACGGTCTC	TACCCTACG	CTGCTGTCCA	AGGAGTTGCC					
AGCGGCAGAC	GATGCCAGAG	ATGGCGATGC	GACGACAGGT	TCCTCAACGG					
755	760	765	770	775	780	785	790	795	800
*	*	*	*	*	*	*	*	*	*
TCGATGGTCT	GCTTCTACGG	AGTTCCGCTT	CTGATTGTCA	ATGGGTTCTT					
AGCTACCAGA	CGAAGATGCC	TCAAGGCGAA	GACTAACAGT	TACCCAAGAA					
805	810	815	820	825	830	835	840	845	850
*	*	*	*	*	*	*	*	*	*
AGTTTGATC	ACTTACTTGC	AGCACACGCA	TCCTTCCCTG	CCTCACTATG					
TCAAAACTAG	TGAATGAAGC	TCGTGTGCGT	AGGAAGGGAC	GGAGTGATAC					
855	860	865	870	875	880	885	890	895	900
*	*	*	*	*	*	*	*	*	*
ACTCGTCTGA	GTGGGATTGG	TTGAGGGAG	CTTGGCCAC	CGTTGACAGA					
TGAGCAGACT	CACCTAACCC	AACTCCCCTC	GAAACCGGTG	GCAACTGTCT					
905	910	915	920	925	930	935	940	945	950
*	*	*	*	*	*	*	*	*	*
GACTACGGAA	TCTTGAACAA	GGTCTTCCAC	AATATCACGG	ACACGCACGT					
CTGATGCCTT	AGAACTTGTG	CCAGAAGGTG	TTATAGTGCC	TGTGCGTGCA					
955	960	965	970	975	980	985	990	995	1000
*	*	*	*	*	*	*	*	*	*
GGCGCATCAC	CTGTTCTCGA	CCATGCCGCA	TTATCATGCG	ATGGAAGCTA					
CCCGCTAGTG	GACAAGAGCT	GGTACGGCGT	AATAGTACGC	TACCTTCGAT					
1005	1010	1015	1020	1025	1030	1035	1040	1045	1050
*	*	*	*	*	*	*	*	*	*
CGAAGGCGAT	AAAGCCGATA	CTGGGAGAGT	ATTATCAGTT	GCATGGGACG					
GCTTCCGCTA	TTTCGGCTAT	GACCCTCTCA	TAATAGTCAA	CGTACCCCTGC					
1055	1060	1065	1070	1075	1080	1085	1090	1095	1100
*	*	*	*	*	*	*	*	*	*
CCGGTGGTTA	AGGCATGTG	GAGGGAGGCG	AAGGAGTGT	TCTATGTGGA					
GGCCACCAAT	TCCGCTACAC	CTCCCTCCGC	TTCCCTCACAT	AGATACACCT					
1105	1110	1115	1120	1125	1130	1135	1140	1145	1150
*	*	*	*	*	*	*	*	*	*
ACCGGACAGG	CAAGGTGAGA	AGAAAGGTGT	GTTCTGGTAC	AACAATAAGT					
TGGCCTGTCC	GTTCCACTCT	TCTTCCACAA	CAAGACCATG	TTGTTATTCA					
1155	1160	1165	1170	*	*				
TATGAAGCAA	AGAAGAAACA	AT							
ATACTTCGTT	TCTTCTTTGT	TA							

Sequence Range: 1 to 1172

	5	10	15	20	25	30	35	40	45						
	*	*	*	*	*	*	*	*	*						
ATG	GGT	GCA	GGT	GGA	AGA	ATG	CAA	GTG	TCT	CCT	CCC	TCC	AAA	AAG	TCT
TAC	CCA	CGT	CCA	CCT	TCT	TAC	GTT	CAC	AGA	GGA	GGG	AGG	TTT	TTC	AGA
M	G	A	G	G	R	M	Q	V	S	P	P	S	K	K	S>
50	55	60	65	70	75	80	85	90	95	*	*	*	*	*	*
GAA	ACC	GAC	AAC	ATC	AAG	CGC	GTA	CCC	TGC	GAG	ACA	CCG	CCC	TTC	ACT
CTT	TGG	CTG	TTG	TAG	TTC	GCG	CAT	GGG	ACG	CTC	TGT	GGC	GGG	AAG	TGA
E	T	D	N	I	K	R	V	P	C	E	T	P	P	F	T>
100	105	110	115	120	125	130	135	140	*	*	*	*	*	*	*
GTC	GGA	GAA	CTC	AAG	AAA	GCA	ATC	CCA	CCG	CAC	TGT	TTC	AAA	CGC	TCG
CAG	CCT	CTT	GAG	TTC	TTT	CGT	TAG	GGT	GGC	GTG	ACA	AAG	TTT	GCG	AGC
V	G	E	L	K	K	A	I	P	P	H	C	F	K	R	S>
145	150	155	160	165	170	175	180	185	190	*	*	*	*	*	*
ATC	CCT	CGC	TCT	TTC	TCC	TAC	CTC	ATC	TGG	GAC	ATC	ATC	ATA	GCC	TCC
TAG	GGA	GCG	AGA	AAG	AGG	ATG	GAG	TAG	ACC	CTG	TAG	TAG	TAT	CGG	AGG
I	P	R	S	F	S	Y	L	I	W	D	I	I	I	A	S>
195	200	205	210	215	220	225	230	235	240	*	*	*	*	*	*
TGC	TTC	TAC	TAC	GTC	GCC	ACC	ACT	TAC	TTC	CCT	CTC	CTC	CCT	CAC	CCT
ACG	AAG	ATG	ATG	CAG	CGG	TGG	TGA	ATG	AAG	GGA	GAG	GAG	GGA	GTG	GGA
C	F	Y	Y	V	A	T	T	Y	F	P	L	L	P	H	P>
245	250	255	260	265	270	275	280	285	*	*	*	*	*	*	*
CTC	TCC	TAC	TTC	GCC	TGG	CCT	CTC	TAC	TGG	GCC	TGC	CAG	GGC	TGC	GTC
GAG	AGG	ATG	AAG	CGG	ACC	GGG	GAG	ATG	ACC	CGG	ACG	GTC	CCG	ACG	CAG
L	S	Y	F	A	W	P	L	Y	W	A	C	Q	G	C	V>
290	295	300	305	310	315	320	325	330	335	*	*	*	*	*	*
CTA	ACC	GGC	GTC	TGG	GTC	ATA	GCC	CAC	AG	TGC	GGC	CAC	CAC	GCC	TTC
GAT	TGG	CCG	CAG	ACC	CAG	TAT	CGG	GTG	TC	ACG	CCG	GTG	GTG	CGG	AAG
L	T	G	V	W	V	I	A	H	<del>C</del>	C	G	H	H	A	F>
340	345	350	355	360	365	370	375	380	*	*	*	*	*	*	*
AGC	GAC	TAC	CAG	TGG	CTG	GAC	GAC	ACC	GTC	GGC	CTC	ATC	TTC	CAC	TCC
TCG	CTG	ATG	GTC	ACC	GAC	CTG	CTG	TGG	CAG	CCG	GAG	TAG	AAG	GTG	AGG
S	D	Y	Q	W	L	D	D	T	V	G	L	I	F	H	S>
385	390	395	400	405	410	415	420	425	430	*	*	*	*	*	*
TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	CGA	CGC	CAC
AAG	GAG	GAG	CAG	GGG	ATG	AAG	AGG	ACC	TTC	ATG	TCA	GTA	GCT	GCG	GTG
F	L	L	V	P	Y	F	S	W	K	Y	S	H	R	R	H>
435	440	445	450	455	460	465	470	475	480	*	*	*	*	*	*
CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	GTC	CCC	AAG
GTA	AGG	TTG	TGA	CCG	AGG	GAG	CTC	TCT	CTG	CTT	CAC	AAA	CAG	GGG	TTC
H	S	N	T	G	S	L	E	R	D	E	V	F	V	P	K>

( found in  
Wild type + 129 F gene)

485	490	495	500	*	505	510	*	515	520	*	525					
AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	GGC	AAG	TAC	CAC					
TTC	TTC	AGT	CTG	TAG	TTC	ACC	ATG	CCG	TTC	ATG	GAG					
K	K	S	D	I	K	W	Y	G	K	Y	N					
											P					
L>																
530	535	540	*	545	*	550	*	555	*	560	*	565	570	*	575	
GGA	CGC	ACC	GTG	ATG	TTA	ACG	GTT	CAG	TTC	ACT	CTC	GGC	TGG	CCT	TTG	
CCT	GGG	TGG	CAC	TAC	AAT	TGC	CAA	GTC	AAG	TGA	GAG	CCG	ACC	GGA	AAC	
G	R	T	V	M	L	T	V	Q	F	T	L	G	W	P	L>	
580	585	590	*	595	*	600	*	605	*	610	*	615	620	*	*	
TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGG	AGA	CCT	TAC	GAC	GGC	GGC	TTC	GCT	
ATG	AAT	CGG	AAG	TTG	CAG	AGC	CCC	TCT	GGA	ATG	CTG	CCG	CCG	AAG	CGA	
Y	L	A	F	N	V	S	G	R	P	Y	D	G	G	F	A>	
625	630	635	*	640	*	645	*	650	*	655	*	660	*	665	670	*
TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC	TAC	AAC	GAC	CGC	GAG	CGT	CTC	
ACG	GTA	AAG	GTG	GGG	TTG	CGA	GGG	TAG	ATG	TTG	CTG	GCG	CTC	GCA	GAG	
C	H	F	H	P	N	A	P	I	Y	N	D	R	E	R	L>	
675	680	685	*	690	*	695	*	700	*	705	*	710	*	715	720	*
CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC	CTC	GCC	GTC	TGC	TAC	GGT	CTC	
GTC	TAT	ATG	TAG	AGG	CTG	CGA	CCG	TAG	GAG	GGG	CAG	ACG	ATG	CCA	GAG	
Q	I	Y	I	S	D	A	G	I	L	A	V	C	Y	G	L>	
725	730	735	*	740	*	745	*	750	*	755	*	760	*	765		
TAC	CGC	TAC	GCT	GTC	CAA	GGG	GTT	GCC	TCG	ATG	GTC	TGC	TTC	TAC		
ATG	GCG	ATG	CGA	CGA	CAG	GTT	CCT	CAA	CGG	AGC	TAC	CAG	ACG	AAG	ATG	
Y	R	Y	A	A	V	Q	G	V	A	S	M	V	C	F	Y>	
770	775	780	*	785	*	790	*	795	*	800	*	805	810	*	815	
GGA	GTT	CCG	CTT	CTG	ATT	GTC	AAT	GGG	TTC	TTA	GTT	TTG	ATC	ACT	TAC	
CCT	CAA	GGC	GAA	GAC	TAA	CAG	TTA	CCC	AAG	AAT	CAA	AAC	TAG	TGA	ATG	
G	V	P	L	L	I	V	N	G	F	L	V	L	I	T	Y>	
820	825	830	*	835	*	840	*	845	*	850	*	855	860	*		
TTG	CAG	CAC	ACG	CAT	CCT	TCC	CTG	CCT	CAC	TAT	GAC	TCG	TCT	GAG	TGG	
AAC	GTC	GTG	TGC	GTA	GGA	AGG	GAC	GGA	GTG	ATA	CTG	AGC	AGA	CTC	ACC	
L	Q	H	T	H	P	S	L	P	H	Y	D	S	S	E	W>	
865	870	875	*	880	*	885	*	890	*	895	*	900	*	905	910	*
GAT	TGG	TTG	AGG	GGA	GCT	TTG	GCC	ACC	GTT	GAC	AGA	GAC	TAC	GGA	ATC	
CTA	ACC	AAC	TCC	CCT	CGA	AAC	CGG	TGG	CAA	CTG	TCT	CTG	ATG	CCT	TAG	
D	W	L	R	G	A	L	A	T	V	D	R	D	Y	G	I>	
915	920	925	*	930	*	935	*	940	*	945	*	950	*	955	960	*
TTG	AAC	AAG	GTC	TTC	CAC	AAT	ATC	ACG	GAC	ACG	CAC	GTG	GCG	CAT	CAC	
AAC	TTG	TTC	CAG	AAG	GTG	TTA	AGG	TGC	CTG	TGC	GTG	CAC	CGC	GTA	GTG	
L	N	K	V	F	H	N	I	T	D	T	H	V	A	H	H>	
965	970	975	*	980	*	985	*	990	*	995	*	1000	1005			

CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT ACG AAG GCG  
GAC AAG AGC TGG TAC GGC GTA ATA GTA CGC TAC CTT CGA TGC TTC CGC  
L F S T M P H Y H A M E A T K A>  
1010 1015 1020 1025 1030 1035 1040 1045 1050 1055  
\* \* \* \* \* \* \* \* \* \*  
ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTG CAT GGG ACG CCG GTG  
TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAC GTA CCC TGC GGC CAC  
I K P I L G E Y Y Q L H G T P V>  
1060 1065 1070 1075 1080 1085 1090 1095 1100  
\* \* \* \* \* \* \* \* \* \*  
GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG  
CAA TTC CGC TAC ACC TCC CTC CGC TTC CTC ACA TAG ATA CAC CTT GGC  
V K A M W R E A K E C I Y V E P>  
1105 1110 1115 1120 1125 1130 1135 1140 1145 1150  
\* \* \* \* \* \* \* \* \* \*  
GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA  
CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT  
D R Q G E K K G V F W Y N N K L>  
1155 1160 1165 1170  
\* \* \* \*  
TGA AGC AAA GAA GAA ACA AT  
ACT TCG TTT CTT CTT TGT TA  
\* S K E E T X>

8:56 AM

5	10	15	20	25	30	35	40	45	50
*	*	*	*	*	*	*	*	*	*
ATGGGTGCAG GTGGAAGAAT GCAAGTGTCT CCTCCCTCCA AGAAGTCTGA TACCCACGTC CACCTTCTTA CGTTCACAGA GGAGGGAGGT TCTTCAGACT									
55	60	65	70	75	80	85	90	95	100
*	*	*	*	*	*	*	*	*	*
AACCAGACACC ATCAAGCGCG TACCCCTGCGA GACACCGCCC TTCACTGTCG TTGGCTGTGG TAGTTCGCGC ATGGGACGCT CTGTGGCGGG AAGTGACAGC									
105	110	115	120	125	130	135	140	145	150
*	*	*	*	*	*	*	*	*	*
GAGAACTCAA GAAAGCAATC CCACCGCACT GTTTCAAACG CTCGATCCCT CTCTTGAGTT CTTTCGTTAG GGTGGCGTGA CAAAGTTTGC GAGCTAGGGA									
155	160	165	170	175	180	185	190	195	200
*	*	*	*	*	*	*	*	*	*
CGCTCTTTCT CCTACCTCAT CTGGGACATC ATCATAGCCT CCTGCTTCTA GCGAGAAAGA GGATGGAGTA GACCCTGTAG TAGTATCGGA GGACGAAGAT									
205	210	215	220	225	230	235	240	245	250
*	*	*	*	*	*	*	*	*	*
CTACNTCGCC ACCACTTACT TCCCTCTCCT CCCTCACCCCT CTCTCCTACT GATGNAGCGG TGGTGAATGA AGGGAGAGGA GGGAGTGGGA GAGAGGATGA									
255	260	265	270	275	280	285	290	295	300
*	*	*	*	*	*	*	*	*	*
TCGCCCTGGCC TCTCTACTGG GCCTGCCAAG GGTGCGTCCT AACCGGGCGTC AGCGGACCGG AGAGATGACC CGGACGGTTC CCACGCAGGA TTGGCCGCAG									
305	310	315	320	325	330	335	340	345	350
*	*	*	*	*	*	*	*	*	*
TGGGTCATAG CCCACAGTG CGGCCACAC GCCTTCAGCG ACTACCAGTG ACCCAGTATC GGGTGTCAC GCGGGTGGT CGGAAGTCGC TGATGGTCAC									
355	360	365	370	375	380	385	390	395	400
*	*	*	*	*	*	*	*	*	*
GCTTGACGAC ACCGTCGGTC TCATCTTCCA CTCCCTCCTC CTCGTCCCTT CGAACTGCTG TGGCAGCCAG AGTAGAAGGT GAGGAAGGAG GAGCAGGGAA									
405	410	415	420	425	430	435	440	445	450
*	*	*	*	*	*	*	*	*	*
ACTTCTCCTG GAAGTACAGT CATCGCAGCC ACCATTCCAA CACTGGCTCC TGAAGAGGAC CTTCATGTCA GTAGCGTCGG TGGTAAGGTT GTGACCGAGG									
455	460	465	470	475	480	485	490	495	500
*	*	*	*	*	*	*	*	*	*
CTCGAGAGAG ACGAAAGTGT TGTCCTTCAAG AAGAAGTCAG ACATCAAGTG GAGCTCTCTC TGCTTCACAA ACAGGGTTC TTCTTCAGTC TGTAGTTCAC									
505	510	515	520	525	530	535	540	545	550
*	*	*	*	*	*	*	*	*	*
GTACGGCAAG TACCTCAACA ACCCTTTGGG ACCGACCGTG ATGTTAACGG CATGCCGTTA ATGGAGTTGT TGGAAACCC TGCGTGGCAC TACAATTGCC									
555	560	565	570	575	580	585	590	595	600
*	*	*	*	*	*	*	*	*	*
TTCAGTTCAC TCTCGGCTGG CCGTTGTACT TAGCTTCATA CGTCTCGGGAA AAGTCAAGTG AGAGCCGACC GGCAACATGA ATCGGAAGTT GCAGAGCCCT									
605	610	615	620	625	630	635	640	645	650
*	*	*	*	*	*	*	*	*	*
AGACCTTACG ACGGCGGCTT CCGTTGCCAT TTCCACCCCCA ACGCTCCCCAT									

8:56 AM

TCTGGAAATGC TGCCGCCGAA GGCAACGGTA AAGGTGGGGT TGCGAGGGTA

655 660 665 670 675 680 685 690 695 700  
 \* \* \* \* \* \* \* \* \* \*

CTACAAACGAC CGCGAGCGTC TCCAGATATA CATCTCCGAC GCTGGCATCC  
 GATGTTGCTG GCGCTCGCAG AGGTCTATAT GTAGAGGGCTG CGACCGTAGG

705 710 715 720 725 730 735 740 745 750  
 \* \* \* \* \* \* \* \* \* \*

TCGCCGTCTG CTACGGTCTC TTCCGTTACG CCGCCGGCCA GGGAGTGGCC  
 AGCGGCAGAC GATGCCAGAG AAGGCAATGC GGCGGCCGGT CCCTCACCGG

755 760 765 770 775 780 785 790 795 800  
 \* \* \* \* \* \* \* \* \* \*

TCGATGGTCT GCTTCTACGG AGTCCCCTT CTGATTGTCA ATGGTTTCCT  
 AGCTACCAGA CGAACATGCC TCAGGGCGAA GACTAACAGT TACCAAAGGA

805 810 815 820 825 830 835 840 845 850  
 \* \* \* \* \* \* \* \* \* \*

CGTGTGATC ACTTACTTGC AGCACACGCA TCCTTCCCTG CCTCACTACG  
 GCACAACTAG TGAATGAACG TCGTGTGCGT AGGAAGGGAC GGAGTGATGC

855 860 865 870 875 880 885 890 895 900  
 \* \* \* \* \* \* \* \* \* \*

ATTCGTCCGA GTGGGATTGG TTCAGGGGAG CTTTGGCTAC CGTTGACAGA  
 TAAGCAGGCT CACCCCTAACCC AAGTCCCCTC GAAACCGATG GCAACTGTCT

905 910 915 920 925 930 935 940 945 950  
 \* \* \* \* \* \* \* \* \* \*

GACTACGGAA TCTTGAACAA GGTCTTCCAC AATATTACCG ACACGCACGT  
 CTGATGCCTT AGAACTTGTG TTATAATGGC TGTGCGTGCA

955 960 965 970 975 980 985 990 995 1000  
 \* \* \* \* \* \* \* \* \* \*

GGCCCATCAT CCGTTCTCCA CGATGCCGCA TTATCACGCG ATGGAAGCTA  
 CGGGGTAGTA GGCAAGAGGT GCTACGGCGT AATAGTGCAC TACCTTCGAT

1005 1010 1015 1020 1025 1030 1035 1040 1045 1050  
 \* \* \* \* \* \* \* \* \* \*

CCAAGGCGAT AAAGCCGATA CTGGGAGAGT ATTATCAGTT CGATGGGACG  
 GGTTCCGCTA TTTCGGCTAT GACCCCTCTCA TAATAGTCAA GCTACCCCTGC

1055 1060 1065 1070 1075 1080 1085 1090 1095 1100  
 \* \* \* \* \* \* \* \* \* \*

CCGGTGGTTA AGGGGATGTG GAGGGAGGCG AAGGAGTGTG TCTATGTGGA  
 GGCCACCAAT TCCGCTACAC CTCCCTCCGC TTCCCTCACAT AGATAACACCT

1105 1110 1115 1120 1125 1130 1135 1140 1145 1150  
 \* \* \* \* \* \* \* \* \* \*

ACCGGACAGG CAAGGTGAGA AGAAAGGTGT GTTCTGGTAC AACAAATAAGT  
 TGGCCTGTCC GTTCCACTCT TCTTTCCACA CAAGACCATG TTGTTATTCA

1155 1160 1165 1170 1175 1180 1185  
 \* \* \* \* \* \* \* \* \*

TATGAGGATA TGATGATGGT GAAAGAAATC ACTAG  
 ATACTCCTAT ACTACTACCA CTTTCTTTAG TGATC

Sequence Range: 1 to 1185

	5	10	15	20	25	30	35	40	45						
	*		*	*	*	*	*	*	*						
ATG	GGT	GCA	GGT	GGA	AGA	ATG	CAA	GTG	TCT	CCT	CCC	TCC	AAG	AAG	TCT
TAC	CCA	CGT	CCA	CCT	TCT	TAC	GTT	CAC	AGA	GGA	GGG	AGG	TTC	TTC	AGA
M	G	A	G	G	R	M	Q	V	S	P	P	S	K	K	S>
50	55	60	65	70	75	80	85	90	95	*	*	*	*	*	
GAA	ACC	GAC	ACC	ATC	AAG	CGC	GTA	CCC	TGC	GAG	ACA	CCG	CCC	TTC	ACT
CTT	TGG	CTG	TGG	TAG	TTC	GCG	CAT	GGG	ACG	CTC	TGT	GGC	GGG	AAG	TGA
E	T	D	T	I	K	R	V	P	C	E	T	P	P	F	T>
100	105	110	115	120	*	125	130	135	140	*	*	*	*	*	
GTC	GGA	GAA	CTC	AAG	AAA	GCA	ATC	CCA	CCG	CAC	TGT	TTC	AAA	CGC	TCG
CAG	CCT	CTT	GAG	TTC	TTT	CGT	TAG	GGT	GGC	GTG	ACA	AAG	TTT	GCG	AGC
V	G	E	L	K	K	A	I	P	P	H	C	F	K	R	S>
145	150	155	160	165	170	*	175	180	185	190	*	*	*	*	
ATC	CCT	CGC	TCT	TTC	TCC	TAC	CTC	ATC	TGG	GAC	ATC	ATC	ATA	GCC	TCC
TAG	GGA	GCG	AGA	AAG	AGG	ATG	GAG	TAG	ACC	CTG	TAG	TAG	TAT	CGG	AGG
I	P	R	S	F	S	Y	L	I	W	D	I	I	I	A	S>
195	200	205	210	*	215	220	*	225	230	*	235	240	*	*	
TGC	TTC	TAC	TAC	NTC	GCC	ACC	ACT	TAC	TTC	CCT	CTC	CTC	CCT	CAC	CCT
ACG	AAG	ATG	ATG	NAG	CGG	TGG	TGA	ATG	AAG	GGA	GAG	GAG	GGA	GTG	GGA
C	F	Y	Y	X	A	T	T	Y	F	P	L	L	P	H	P>
245	250	255	260	*	265	270	*	275	280	*	285	*	*	*	
CTC	TCC	TAC	TTC	GCC	TGG	CCT	CTC	TAC	TGG	GCC	TGC	CAA	GGG	TGC	GTC
GAG	AGG	ATG	AAG	CGG	ACC	GGG	GAG	ATG	ACC	CGG	ACG	GTT	CCC	ACG	CAG
L	S	Y	F	A	W	P	L	Y	W	A	C	Q	G	C	V>
290	295	300	305	*	310	*	315	320	*	325	330	*	*	*	
CTA	ACC	GGC	GTC	TGG	GTC	ATA	GCC	CAC	AAG	TGC	GGC	CAC	CAC	GCC	TTC
GAT	TGG	CCG	CAG	ACC	CAG	TAT	CGG	GTG	TTC	ACG	CCG	GTG	GTG	CGG	AAG
L	T	G	V	W	V	I	A	H	<del>C</del>	C	G	H	H	A	F>
340	345	350	355	*	360	*	365	370	*	375	380	*	*	*	
AGC	GAC	TAC	CAG	TGG	CTT	GAC	GAC	ACC	GTC	GGT	CTC	ATC	TTC	CAC	TCC
TCG	CTG	ATG	GTC	ACC	GAA	CTG	CTG	TGG	CAG	CCA	GAG	TAG	AAG	GTG	AGG
S	D	Y	Q	W	L	D	D	T	V	G	L	I	F	H	S>
385	390	395	400	*	405	410	*	415	420	*	425	430	*	*	
TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	CGC	AGC	CAC
AAG	GAG	GAG	CAG	GGA	ATG	AAG	AGG	ACC	TTC	ATG	TCA	GTA	GCG	TCG	GTG
F	L	L	V	P	Y	F	S	W	K	Y	S	H	R	S	H>
435	440	445	450	*	455	460	*	465	470	*	475	480	*	*	
CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	GTC	CCC	AAG
GTA	AGG	TTC	TGA	CCG	AGG	GAG	CTC	TCT	CTG	CTT	CAC	AAA	CAG	GGG	TTC
H	S	N	T	G	S	L	E	R	D	E	V	F	V	P	K>

485	490	495	500	*	505	510	*	515	520	*	525				
AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	GGC	AAG	TAC	CTC	AAC	AAC	CCT	TTG
TTC	TTC	AGT	CTG	TAG	TTC	ACC	ATG	CCG	TTC	ATG	GAG	TTG	TTG	GGA	AAC
K	K	S	D	I	K	W	Y	G	K	Y	L	N	N	P	L>
530	535	540	*	545	*	550	*	555	*	560	*	565	570	*	575
GGA	CGC	ACC	GTG	ATG	TTA	ACG	GTT	CAG	TTC	ACT	CTC	GGC	TGG	CCG	TTG
CCT	GCG	TGG	CAC	TAC	AAT	TGC	CAA	GTC	AAG	TGA	GAG	CCG	ACC	GGC	AAC
G	R	T	V	M	L	T	V	Q	F	T	L	G	W	P	L>
580	585	590	*	595	*	600	*	605	*	610	*	615	620	*	
TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGG	AGA	CCT	TAC	GAC	GGC	GGC	TTC	CGT
ATG	AAT	CGG	AAG	TTG	CAG	AGC	CCT	TCT	GGA	ATG	CTG	CCG	CCG	AAG	GCA
Y	L	A	F	N	V	S	G	R	P	Y	D	G	G	F	R>
625	630	635	*	640	*	645	*	650	*	655	*	660	665	670	*
TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC	TAC	AAC	GAC	CGC	GAG	CGT	CTC
ACG	GTA	AAG	GTG	GGG	TTG	CGA	GGG	TAG	ATG	TTG	CTG	GCG	CTC	GCA	GAG
C	H	F	H	P	N	A	P	I	Y	N	D	R	E	R	L>
675	680	685	*	690	*	695	*	700	*	705	*	710	*	715	720
CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC	CTC	GCC	GTC	TGC	TAC	GGT	CTC
GTC	TAT	ATG	TAG	AGG	CTG	CGA	CCG	TAG	GAG	CGG	CAG	ACG	ATG	CCA	GAG
Q	I	Y	I	S	D	A	G	I	L	A	V	C	Y	G	L>
725	730	735	*	740	*	745	*	750	*	755	*	760	*	765	
TTC	CGT	TAC	GCC	GCC	GGC	CAG	GGG	GTG	GCC	TCG	ATG	GTC	TGC	TTC	TAC
AAG	GCA	ATG	CGG	CGG	CCG	GTC	CCT	CAC	CGG	AGC	TAC	CAG	ACG	AAG	ATG
F	R	Y	A	A	G	Q	G	V	A	S	M	V	C	F	Y>
770	775	780	*	785	*	790	*	795	*	800	*	805	810	*	815
GGA	GTC	CCG	CTT	CTG	ATT	GTC	AAT	GGT	TTC	CTC	GTG	TTG	ATC	ACT	TAC
CCT	CAG	GGC	GAA	GAC	TAA	CAG	TTA	CCA	AAG	GAG	CAC	AAC	TAG	TGA	ATG
G	V	P	L	L	I	V	N	G	F	L	V	L	I	T	Y>
820	825	830	*	835	*	840	*	845	*	850	*	855	860	*	
TTG	CAG	CAC	ACG	CAT	CCT	TCC	CTG	CCT	CAC	TAC	GAT	TCG	TCC	GAG	TGG
AAC	GTC	GTG	TGC	GTA	GGA	AGG	GAC	GGA	GTG	ATG	CTA	AGC	AGG	CTC	ACC
L	Q	H	T	H	P	S	L	P	H	Y	D	S	S	E	W>
865	870	875	*	880	*	885	*	890	*	895	*	900	*	905	910
GAT	TGG	TTC	AGG	GGA	GCT	TTG	GCT	ACC	GTT	GAC	AGA	GAC	TAC	GGA	ATC
CTA	ACC	AAG	TCC	CCT	CGA	AAC	CGA	TGG	CAA	CTG	TCT	CTG	ATG	CCT	TAG
D	W	F	R	G	A	L	A	T	V	D	R	D	Y	G	I>
915	920	925	*	930	*	935	*	940	*	945	*	950	*	955	960
TTG	AAC	AAG	GTC	TTC	CAC	AAT	ATT	ACC	GAC	ACG	CAC	GTG	GCC	CAT	CAT
AAC	TTG	TTC	CAG	AAG	GTG	TTA	TAA	TGG	CTG	TGC	GTG	CAC	CGG	GTA	GTA
L	N	K	V	F	H	N	I	T	D	T	H	V	A	H	H>
965	970	975	*	980	*	985	*	990	*	995	*	1000	*	1005	

CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG  
GGC AAG AGG TGC TAC GGC GTA ATA GTG CGC TAC CTT CGA TGG TTC CGC  
P F S T M P H Y H A M E A T K A>  
1010 1015 1020 1025 1030 1035 1040 1045 1050 1055  
\* \* \* \* \* \* \* \* \* \*  
ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG  
TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAG CTA CCC TGC GGC CAC  
I K P I L G E Y Y Q F D G T P V>  
1060 1065 1070 1075 1080 1085 1090 1095 1100  
\* \* \* \* \* \* \* \* \* \*  
GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG  
CAA TTC CGC TAC ACC TCC CTC CGC TTC CTC ACA TAG ATA CAC CTT GGC  
V K A M W R E A K E C I Y V E P>  
1105 1110 1115 1120 1125 1130 1135 1140 1145 1150  
\* \* \* \* \* \* \* \* \* \*  
GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA  
CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT  
D R Q G E K K G V F W Y N N N K L>  
1155 1160 1165 1170 1175 1180 1185  
\* \* \* \* \* \* \* \* \* \*  
TGA GGA TAT GAT GAT GGT GAA AGA AAT CAC TAG  
ACT CCT ATA CTA CTA CCA CTT TCT TTA GTG ATC  
\* G Y D D G E R N H \*>